

FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT
CCAACCATTCCTCCCTTGAGTTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCACCCGGA
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCCTTCAGCCT
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC
CTGCCACCCCTCAACGTCTCTAATGGCTCTGACGCCCGCTGCCCTGCACCTTCAACTCCTGC
TACACAGTGAACCACAAACAGTTCTCCCTGAACCTGGACTTACCAGGAGTGCAACAACCTGCTC
TGAGGAGATGTTCTCCAGTTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG
ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTCCGTGATGCTGAGAAACGTG
CAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCTTGACCGCCACCGTGG
CCATGGCAAGATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGAGCTCCACGGGTGG
CCGTGATTGTGGGTGCCCTCCGTGGGGGCTTCTGGCTGTGGTCACTCTTGGTGCTGATGGTG
GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCAGAGATGACCTGAAGACCGAGGA
GGAGGGCAAGACGGACGGTGAAGGCCAACCCGGATGATGGCGCCAAGTAGGGGTGGCCGGCC
CTGCAGCCTCCCGTGTCCGTCTCCTCCCTCTCCGCCCTGTACAGTGACCTGCCTGCTCG
CTCTTGGTGCTTCCCGTGACCTAGGACCCAGGGCCCACTGGGGCCTCCTGAACCCCG
ACTTCGTATCTCCACCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCCACTGCCAGTCCCTGG
GGGAGGCGAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGCGAGGGGTAGA
GGAGGGGCCGTGTACCTGCCAGTGTCTTGCTGGCAGTGGCTTCAGAGAGGACCTGGTGG
GGAGGGAGGGCTTTCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG
TGCTCTCCCTGTCTCCAGCCCGAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTGA
AACTTTGAGGGGATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAGCCAGGG
GTGCAGGCAAGCTGGACATGTGCCTGGCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCAGCGGGGACCCACCAAGAGGGCC
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTGTCTGCA
GCTCTGCTTCTCCATGGGGTAACACCCCTCGCTGGGCAGGGGCGACCAAGGCTGGGAAAT
GAGGAGGCCATGCACAGGGTGGGGCAGCTTCTTTGGGGCTTCAGTGAGAACTCTCCAGTT
GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGGAAGGGAAGCCTGAGGCCG
GCATAAGGGGAGGCCTTGGAACCTGAGCTGCCAATGCCAGCCCTGTCCATCTGCGGCCACG
CTACTCGTCTCTCCCAACAACCTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC
ACAGTGGCTCAGCCTGTAAATCCAGCACCTTTGGGAGGCCAAGGCGGGTGGATTACCTCCAT
CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG
GTGGCGTGTGCTGTAAATCCAGCTATTGGGAGGGCTGAGGCAGGAGAATCGCTTGAGCCCG
GGAAGCAGAGTTGTCAGTGAACCTGAGATAGTAGTGCCTGCAATTACAGCCTGGGTGAC
ATAGAGAGACTCCATCTCAAAAAAA

09378295-103504

FIGURE 55

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

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FSLNWTYQECNNCSEEMFLQFRMKI INLKLERFQDRVEFSGNPSKYDVSVMRLRNVQPEDEGI
YNCYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRVK
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

007325-4040

FIGURE 56

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCGCCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTTCTCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG
TTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
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TTTACAAC TGCTACATCATGAACCCCC

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